N/A
Sector 1804

PAGE: 1

RAW SEQUENCE LISTING
PATENT APPLICATION *US/08/799,910*

DATE: 11/26/97
TIME: 13:57:20

INPUT SET: S21738.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

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 1                          SEQUENCE LISTING
 2
 3   (1)    General Information
 4
 5          (i) APPLICANT: Falb, Dean
 6
 7          (ii) TITLE OF THE INVENTION: COMPOSITIONS AND METHODS FOR
 8                   THE TREATMENT AND DIAGNOSIS OF
 9                   CARDIOVASCULAR DISEASE
10
11          (iii) NUMBER OF SEQUENCES: 44
12
13          (iv) CORRESPONDENCE ADDRESS:
14             (A) ADDRESSEE: PENNIE & EDMONDS LLP
15             (B) STREET: 1155 Avenue of the Americas
16             (C) CITY: New York
17             (D) STATE: NY
18             (E) COUNTRY: USA
19             (F) ZIP: 10036-2711
20
21          (v) COMPUTER READABLE FORM:
22             (A) MEDIUM TYPE: Diskette
23             (B) COMPUTER: IBM Compatible
24             (C) OPERATING SYSTEM: DOS
25             (D) SOFTWARE: FastSEQ Version 2.0
26
27          (vi) CURRENT APPLICATION DATA:
28             (A) APPLICATION NUMBER: 08/799,910
29             (B) FILING DATE: 13-FEB-1997
30             (C) CLASSIFICATION:
31
32          (vii) PRIOR APPLICATION DATA:
33             (A) APPLICATION NUMBER: 60/011,787
34             (B) FILING DATE: 16-FEB-1996
35
36
37
38          (viii) ATTORNEY/AGENT INFORMATION:
39             (A) NAME: Coruzzi, Laura A
40             (B) REGISTRATION NUMBER: 30,742
41             (C) REFERENCE/DOCKET NUMBER: 7853-067-999
42
43          (ix) TELECOMMUNICATION INFORMATION:
44             (A) TELEPHONE: (212)7909090
45             (B) TELEFAX: (212)8699741
46             (C) TELEX: 66141 PENNIE
```

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47
48
49               (2) INFORMATION FOR SEQ ID NO:1:
50
51         (i) SEQUENCE CHARACTERISTICS:
52            (A) LENGTH: 1953 base pairs
53            (B) TYPE: nucleic acid
54            (C) STRANDEDNESS: both
55            (D) TOPOLOGY: linear
56
57         (ii) MOLECULE TYPE: cDNA
58         (ix) FEATURE:
59
60            (A) NAME/KEY: Coding Sequence
61            (B) LOCATION: 162...1871
62            (D) OTHER INFORMATION:
63
64
65         (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
66
67  GGCACGAGTC GGAGCCGGGC GGAGGGGAGG GGGGAAAGAG GAGCGCAGGG TGAGAGTGAG        60
68  CCGCAGGCTT CGGGAGGCGA GGGGGCGGGG GGAGCAGCGC CGAGGYCGCC GCCTCCGCCT       120
69  CCGCCGCCTA GGACTAGGGG GTGGGGGACG GACAAGCCCC G ATG CCG GGG GAG ACG       176
70                                                Met Pro Gly Glu Thr
71                                                 1               5
72
73  GAA GAG CCG AGA CCC CCG GAG CAG CAG GAC CAG GAA GGG GGA GAG GCG         224
74  Glu Glu Pro Arg Pro Pro Glu Gln Gln Asp Gln Glu Gly Gly Glu Ala
75              10                  15                  20
76
77  GCC AAG GCG GCT CCG GAG GAG CCC CAA CAA CGG CCC CCT GAG GCG GTC         272
78  Ala Lys Ala Ala Pro Glu Glu Pro Gln Gln Arg Pro Pro Glu Ala Val
79          25                  30                  35
80
81  GCG GCG GCG CCT GCA GGG ACC ACT AGC AGC CGC GTG CTG AGG GGA GGT         320
82  Ala Ala Ala Pro Ala Gly Thr Thr Ser Ser Arg Val Leu Arg Gly Gly
83          40                  45                  50
84
85  CGG GAC CGA GGC CGG GCC GCT GCG GCC GCC GCC GCC GCA GCT GTG TCC         368
86  Arg Asp Arg Gly Arg Ala Ala Ala Ala Ala Ala Ala Ala Val Ser
87      55                  60                  65
88
89  CGC CGG AGG AAG GCC GAG TAT CCC CGC CGG CGG AGG AGC AGC CCC AGC         416
90  Arg Arg Arg Lys Ala Glu Tyr Pro Arg Arg Arg Arg Ser Ser Pro Ser
91  70                  75                  80                  85
92
93  GCC AGG CCT CCC GAC GTC CCC GGG CAG CAG CCC CAG GCC GCG AAG TCC         464
94  Ala Arg Pro Pro Asp Val Pro Gly Gln Gln Pro Gln Ala Ala Lys Ser
95                  90                  95                  100
96
97  CCG TCT CCA GTT CAG GGC AAG AAG AGT CCG CGA CTC CTA TGC ATA GAA         512
98  Pro Ser Pro Val Gln Gly Lys Lys Ser Pro Arg Leu Leu Cys Ile Glu
99                  105                 110                 115
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RAW SEQUENCE LISTING
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100
101   AAA GTA ACA ACT GAT AAA GAT CCC AAG GAA GAA AAA GAG GAA GAA GAC      560
102   Lys Val Thr Thr Asp Lys Asp Pro Lys Glu Glu Lys Glu Glu Glu Asp
103           120             125             130
104
105   GAT TCT GCC CTC CCT CAG GAA GTT TCC ATT GCT GCA TCT AGA CCT AGC      608
106   Asp Ser Ala Leu Pro Gln Glu Val Ser Ile Ala Ala Ser Arg Pro Ser
107           135             140             145
108
109   CGG GGC TGG CGT AGT AGT AGG ACA TCT GTT TCT CGC CAT CGT GAT ACA      656
110   Arg Gly Trp Arg Ser Ser Arg Thr Ser Val Ser Arg His Arg Asp Thr
111   150             155             160             165
112
113   GAG AAC ACC CGA AGC TCT CGG TCC AAG ACC GGT TCA TTG CAG CTC ATT      704
114   Glu Asn Thr Arg Ser Ser Arg Ser Lys Thr Gly Ser Leu Gln Leu Ile
115                   170             175             180
116
117   TGC AAG TCA GAA CCA AAT ACA GAC CAA CTT GAT TAT GAT GTT GGA GAA      752
118   Cys Lys Ser Glu Pro Asn Thr Asp Gln Leu Asp Tyr Asp Val Gly Glu
119                   185             190             195
120
121   GAG CAT CAG TCT CCA GGT GGC ATT AGT GGT GAA GAG GAA GAG GAG GAG      800
122   Glu His Gln Ser Pro Gly Gly Ile Ser Gly Glu Glu Glu Glu Glu Glu
123                   200             205             210
124
125   GAA GAA GAG ATG TTA ATC AGT GAA GAG GAG ATA CCA TTC AAA GAT GAT      848
126   Glu Glu Glu Met Leu Ile Ser Glu Glu Glu Ile Pro Phe Lys Asp Asp
127           215             220             225
128
129   CCA AGA GAT GAG ACC TAC AAA CCC CAC TTA GAA AGG GAA ACC CCA AAG      896
130   Pro Arg Asp Glu Thr Tyr Lys Pro His Leu Glu Arg Glu Thr Pro Lys
131   230             235             240             245
132
133   CCA CGG AGA AAA TCA GGG AAG GTA AAA GAA GAG AAG GAG AAG AAG GAA      944
134   Pro Arg Arg Lys Ser Gly Lys Val Lys Glu Glu Lys Glu Lys Lys Glu
135                   250             255             260
136
137   ATT AAA GTG GAA GTA GAG GTG GAG GTG AAA GAA GAG GAG AAT GAA ATT      992
138   Ile Lys Val Glu Val Glu Val Glu Val Lys Glu Glu Glu Asn Glu Ile
139           265             270             275
140
141   AGA GAG GAT GAG GAA CCT CCA AGG AAG AGA GGA AGA AGA CGA AAA GAT     1040
142   Arg Glu Asp Glu Glu Pro Pro Arg Lys Arg Gly Arg Arg Arg Lys Asp
143           280             285             290
144
145   GAC AAA AGT CCA CGT TTA CCC AAA AGG AGA AAA AAG CCT CCA ATC CAG     1088
146   Asp Lys Ser Pro Arg Leu Pro Lys Arg Arg Lys Lys Pro Pro Ile Gln
147           295             300             305
148
149   TAT GTC CGT TGT GAG ATG GAA GGA TGT GGA ACT GTC CTT GCC CAT CCT     1136
150   Tyr Val Arg Cys Glu Met Glu Gly Cys Gly Thr Val Leu Ala His Pro
151   310             315             320             325
152
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153    CGC TAT TTG CAG CAC CAC ATT AAA TAC CAG CAT TTG CTG AAG AAG AAA    1184
154    Arg Tyr Leu Gln His His Ile Lys Tyr Gln His Leu Leu Lys Lys Lys
155            330             335             340
156
157    TAT GTA TGT CCC CAT CCC TCC TGT GGA CGA CTC TTC AGG CTT CAG AAG    1232
158    Tyr Val Cys Pro His Pro Ser Cys Gly Arg Leu Phe Arg Leu Gln Lys
159            345             350             355
160
161    CAA CTT CTG CGA CAT GCC AAA CAT CAT ACA GAT CAA AGG GAT TAT ATC    1280
162    Gln Leu Leu Arg His Ala Lys His His Thr Asp Gln Arg Asp Tyr Ile
163            360             365             370
164
165    TGT GAA TAT TGT GCT CGG GCC TTC AAG AGT TCC CAC AAT CTG GCA GTG    1328
166    Cys Glu Tyr Cys Ala Arg Ala Phe Lys Ser Ser His Asn Leu Ala Val
167            375             380             385
168
169    CAC CGG ATG ATT CAC ACT GGC GAG AAG CCA TTA CAA TGT GAG ATC TGT    1376
170    His Arg Met Ile His Thr Gly Glu Lys Pro Leu Gln Cys Glu Ile Cys
171    390             395             400             405
172
173    GGA TTT ACT TGT CGA CAA AAG GCA TCT CTT AAT TGG CAC ATG AAG AAA    1424
174    Gly Phe Thr Cys Arg Gln Lys Ala Ser Leu Asn Trp His Met Lys Lys
175            410             415             420
176
177    CAT GAT GCA GAC TCC TTC TAC CAG TTT TCT TGC AAT ATC TGT GGC AAA    1472
178    His Asp Ala Asp Ser Phe Tyr Gln Phe Ser Cys Asn Ile Cys Gly Lys
179            425             430             435
180
181    AAA TTT GAG AAG AAG GAC AGC GTA GTG GCA CAC AAG GCA AAA AGC CAC    1520
182    Lys Phe Glu Lys Lys Asp Ser Val Val Ala His Lys Ala Lys Ser His
183            440             445             450
184
185    CCT GAG GTG CTG ATT GCA GAA GCT CTG GCT GCC AAT GCA GGC GCC CTC    1568
186    Pro Glu Val Leu Ile Ala Glu Ala Leu Ala Ala Asn Ala Gly Ala Leu
187            455             460             465
188
189    ATC ACC AGC ACA GAT ATC TTG GGC ACT AAC CCA GAG TCC CTG ACG CAG    1616
190    Ile Thr Ser Thr Asp Ile Leu Gly Thr Asn Pro Glu Ser Leu Thr Gln
191    470             475             480             485
192
193    CCT TCA GAT GGT CAG GGT CTT CCT CTT CTT CCT GAG CCC TTG GGA AAC    1664
194    Pro Ser Asp Gly Gln Gly Leu Pro Leu Leu Pro Glu Pro Leu Gly Asn
195            490             495             500
196
197    TCA ACC TCT GGA GAG TGC CTA CTG TTA GAA GCT GAA GGG ATG TCA AAG    1712
198    Ser Thr Ser Gly Glu Cys Leu Leu Leu Glu Ala Glu Gly Met Ser Lys
199            505             510             515
200
201    TCA TAC TGC AGT GGG ACG GAA CGG GTG AGC CTG ATG GCT GAT GGG AAG    1760
202    Ser Tyr Cys Ser Gly Thr Glu Arg Val Ser Leu Met Ala Asp Gly Lys
203            520             525             530
204
205    ATC TTT GTG GGA AGC GGC AGC AGT GGA GGC ACT GAA GGG CTG GTT ATG    1808
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INPUT SET: S21738.raw

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206    Ile Phe Val Gly Ser Gly Ser Ser Gly Gly Thr Glu Gly Leu Val Met
207        535             540             545

208
209    AAC TCA GAT ATA CTC GGT GCT ACC ACA GAG GTT CTG ATT GAA GAT TCA        1856
210    Asn Ser Asp Ile Leu Gly Ala Thr Thr Glu Val Leu Ile Glu Asp Ser
211    550             555             560             565

212
213    GAC TCT GCC GGA CCT TAGTGGACAG GAAGACTTGG GGCATGGGAC AGCTCAGACT T  1912
214    Asp Ser Ala Gly Pro
215                    570

216
217    TGTATTTAAA AGTTAAAAAG GACAAAAAAA AAAAAAAAAA A                          1953

218
219            (2) INFORMATION FOR SEQ ID NO:2:
220
221            (i) SEQUENCE CHARACTERISTICS:
222                (A) LENGTH: 570 amino acids
223                (B) TYPE: amino acid
224                (C) STRANDEDNESS: unknown
225                (D) TOPOLOGY: unknown
226
227            (ii) MOLECULE TYPE: protein
228            (v) FRAGMENT TYPE: internal
229
230            (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
231
232    Met Pro Gly Glu Thr Glu Glu Pro Arg Pro Pro Glu Gln Gln Asp Gln
233    1               5               10              15
234    Glu Gly Gly Glu Ala Ala Lys Ala Ala Pro Glu Glu Pro Gln Gln Arg
235                20              25              30
236    Pro Pro Glu Ala Val Ala Ala Ala Pro Ala Gly Thr Thr Ser Ser Arg
237            35              40              45
238    Val Leu Arg Gly Gly Arg Asp Arg Gly Arg Ala Ala Ala Ala Ala Ala
239        50              55              60
240    Ala Ala Ala Val Ser Arg Arg Arg Lys Ala Glu Tyr Pro Arg Arg Arg
241    65              70              75              80
242    Arg Ser Ser Pro Ser Ala Arg Pro Pro Asp Val Pro Gly Gln Gln Pro
243                85              90              95
244    Gln Ala Ala Lys Ser Pro Ser Pro Val Gln Gly Lys Lys Ser Pro Arg
245                100             105             110
246    Leu Leu Cys Ile Glu Lys Val Thr Thr Asp Lys Asp Pro Lys Glu Glu
247            115             120             125
248    Lys Glu Glu Glu Asp Asp Ser Ala Leu Pro Gln Glu Val Ser Ile Ala
249        130             135             140
250    Ala Ser Arg Pro Ser Arg Gly Trp Arg Ser Ser Arg Thr Ser Val Ser
251    145             150             155             160
252    Arg His Arg Asp Thr Glu Asn Thr Arg Ser Ser Arg Ser Lys Thr Gly
253                165             170             175
254    Ser Leu Gln Leu Ile Cys Lys Ser Glu Pro Asn Thr Asp Gln Leu Asp
255                180             185             190
256    Tyr Asp Val Gly Glu Glu His Gln Ser Pro Gly Gly Ile Ser Gly Glu
257                195             200             205
258    Glu Glu Glu Glu Glu Glu Glu Glu Met Leu Ile Ser Glu Glu Glu Ile
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SEQUENCE VERIFICATION REPORT
PATENT APPLICATION *US/08/799,910*

Line	Error	Original Text